

P. Mertz



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/684,383

DATE: 06/06/2002
TIME: 16:17:16

Input Set : N:\Crf3\RULE60\09684383.raw
Output Set: N:\CRF3\06062002\I684383.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: H TTEN, Gertrud
6 NEIDHARDT, Helge
7 BECHTOLD, Rolf
8 POHL, Jens
9 PAULISTA, Michael

11 (ii) TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
12 TGF- FAMILY

14 (iii) NUMBER OF SEQUENCES: 49

16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
18 (B) STREET: 655 Fifteenth Street, N. W., G Street Lobby,
19 Suite 330

20 (C) CITY: Washington

21 (D) STATE: DC

22 (E) COUNTRY: USA

23 (F) ZIP: 20005

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/09/684,383
32 (B) FILING DATE: 10-Oct-2000

ENTERED

C--> 32 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/09/218,176

38 (B) FILING DATE:

41 (A) APPLICATION NUMBER: 08/679,048

42 (B) FILING DATE: 12-JUL-1996

46 (A) APPLICATION NUMBER: PCT/EP96/03065

47 (B) FILING DATE: 12-JUL-1996

50 (A) APPLICATION NUMBER: PCT/EP93/00350

51 (B) FILING DATE: 2-FEB-1993

54 (A) APPLICATION NUMBER: US 08/482,577

55 (B) FILING DATE: 7-JUN-1995

58 (A) APPLICATION NUMBER: EP 92 102 324.8

59 (B) FILING DATE: 12-FEB-1992

62 (A) APPLICATION NUMBER: DE P 44 23 190.3

63 (B) FILING DATE: 01-JUL-1994

66 (A) APPLICATION NUMBER: DE 195 11 243.1

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Input Set : N:\CrF3\RULE60\09684383.raw
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67 (B) FILING DATE: 27-MAR-1995
 70 (viii) ATTORNEY/AGENT INFORMATION:
 71 (A) NAME: KITTS, Monica Chin
 72 (B) REGISTRATION NUMBER: 36,105
 73 (C) REFERENCE/DOCKET NUMBER: P564-6010
 75 (ix) TELECOMMUNICATION INFORMATION:
 76 (A) TELEPHONE: 202/638-5000
 77 (B) TELEFAX: 202/638-4810
 79 (2) INFORMATION FOR SEQ ID NO: 1:
 80 (i) SEQUENCE CHARACTERISTICS:
 81 (A) LENGTH: 2272 base pairs
 82 (B) TYPE: nucleic acid
 83 (C) STRANDEDNESS: single
 84 (D) TOPOLOGY: linear
 W--> 86 (ii) MOLECULE TYPE: DNA
 90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 92 CAAGGAGCCA TGCCAGCTGG ACACACACTT CTTCCAGGGC CTCTGGCAGC CAGGACAGAG 60
 94 TTGAGACCAC AGCTGTTGAG ACCCTGAGCC CTGAGTCTGT ATTGCTCAAG AAGGGCCTTC 120
 96 CCCAGCAATG ACCTCCTCAT TGCTTCTGGC CTTTCTCCTC CTGGCTCCAA CCACAGTGGC 180
 98 CACTCCCAGA GCTGGCGGTC AGTGTCCAGC ATGTGGGGGG CCCACCTTGG AACTGGAGAG 240
 100 CCAGCGGGAG CTGCTTCTTG ATCTGGCCAA GAGAACATC TTGGACAAGC TGCACCTCAC 300
 102 CCAGCGCCCA ACACTGAACC GCCCTGTGTC CAGAGCTGCT TTGAGGACTG CACTGCAGCA 360
 104 CCTCCACGGG GTCCACAGG GGGCACTTCT AGAGGACAAAC AGGGAACAGG AATGTGAAAT 420
 106 CATCAGCTT GCTGAGACAG GCCTCTCCAC CATCAACCAG ACTCGTCTTG ATTTTCACTT 480
 108 CTCCTCTGAT AGAACTGCTG GTGACAGGGG GGTCCAGCAG GCCAGTCTCA TGTTCTTTGT 540
 110 GCAGCTCCCT TCCAATACCA CTTGGACCTT GAAAGTGAGA GTCCCTGTGC TGGGTCCACA 600
 112 TAATAACCAAC CTCACCTTGG CTACTCAGTA CCTGCTGGAG GTGGATGCCA GTGGCTGGCA 660
 114 TCAACTCCCC CTAGGGCCTG AAGCTCAAGC TGCCCTGCAGC CAGGGGCACC TGACCCCTGGA 720
 116 GCTGGTACTT GAAGGCCAGG TAGCCCAGAG CTCAGTCATC CTGGGTGGAG CTGCCCATAG 780
 118 GCCTTTGTG GCAGCCCGGG TGAGAGTTGG GGGCAAACAC CAGATTCAAC GACGAGGCAT 840
 120 CGACTGCCAA GGAGGGTCCA GGATGTGCTG TCGACAAGAG TTTTTGTGG ACTTCCGTGA 900
 122 GATTGGCTGG CACGACTGGA TCATCCAGCC TGAGGGCTAC GCCATGAAC TCTGCATAGG 960
 124 GCAGTGCCCA CTACACATAG CAGGCATGCC TGGTATTGCT GCCTCCTTTC ACACTGCAGT 1020
 126 GCTCAATCTT CTCAAGGCCA ACACAGCTGC AGGCACCACT GGAGGGGGCT CATGCTGTGT 1080
 128 ACCCACGGCC CGGGCCCCC TGTCTCTGCT CTATTATGAC AGGGACAGCA ACATTGTCAA 1140
 130 GACTGACATA CCTGACATGG TAGTAGAGGC CTGTGGGTGC AGTTAGTCTA TGTGTGGTAT 1200
 132 GGGCAGCCA AGGTTGCATG GGAAAACACG CCCCTACAGA AGTGCACTTC CTTGAGAGGA 1260
 134 GGGAAATGACC TCATTCTCTG TCCAGAATGT GGACTCCCTC TTCTGAGCA TCTTATGGAA 1320
 136 ATTACCCAC CTTGACTTG AAGAAACCTT CATCTAAAGC AAGTCACTGT GCCATCTTCC 1380
 138 TGACCACTAC CCTCTTCCCT AGGGCATAGT CCATCCCGCT AGTCCATCCC GCTAGCCCCA 1440
 140 CTCCAGGGAC TCAGACCCAT CTCCAACCAT GAGCAATGCC ATCTGGTTCC CAGGCAAAGA 1500
 142 CACCCCTAGC TCACCTTAA TAGACCCCAT AACCCACTAT GCCTTCTGT CCTTTCTACT 1560
 144 CAATGGTCCC CACTCCAAGA TGAGTTGACA CAACCCCTTC CCCCAATTTC TGTGGATCTC 1620
 146 CAGAGAGGCC CTTCTTGGG TTCACCAAAG TTTAGATCAC TGCTGCCAA AATAGAGGCT 1680
 148 TACCTACCCC CCTCTTGTGTT GTGAGCCCT GTCCCTCTTA GTTGTCCAGG TGAACACTA 1740
 150 AAGCTCTCTT TGCATACCTT CATCCATTTC TTGCTCTTCT CTGCCTTCT CTATGCCCTT 1800
 152 AAGGGGTGAC TTGCTGAGC TCTATCACCT GAGCTCCCT GCCCTCTGGC TTCTGCTGA 1860
 154 GGTCAAGGCCA TTTCTTATCC CTGTTCCCTC TCTGTCTAGG TGTCATGGTT CTGTGTAACT 1920
 156 GTGGCTATTTC TGTGTCCCTA CACTACCTGG CTACCCCCCTT CCATGGCCCC AGCTCTGCCT 1980

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158	ACATTCTGAT	TTTTTTTTT	TTTTTTTTTGAAAGTTA	AAAATTCCCTT	AATTTTTAT	2040											
160	TCCTGGTACC	ACTACCACAA	TTTACAGGGC	AATATACTG	ATGTAATGAA	2100											
162	AAAAGACAAA	GCTACAACAG	ATAAAAGACC	TCAGGAATGT	ACATCTAATT	2160											
164	TGCATTAATC	AATAGCTGCA	CTTTTGC	ACTGTGGCTA	TGACAGTCCT	2220											
166	GGTTCCCTGT	TTAACGCTGCA	GTAAC	TGACTATGGA	TCATCGTTCC	2272											
168	(2) INFORMATION FOR SEQ ID NO: 2:																
170	(i) SEQUENCE CHARACTERISTICS:																
171	(A) LENGTH: 352 amino acids																
172	(B) TYPE: amino acid																
173	(C) STRANDEDNESS: single																
174	(D) TOPOLOGY: linear																
176	(ii) MOLECULE TYPE: peptide																
179	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:																
181	Met	Thr	Ser	Ser	Leu	Leu	Leu	Ala	Phe	Leu	Leu	Leu	Ala	Pro	Thr	Thr	
182	1				5					10						15	
184	Val	Ala	Thr	Pro	Arg	Ala	Gly	Gly	Gln	Cys	Pro	Ala	Cys	Gly	Gly	Pro	
185					20				25						30		
187	Thr	Leu	Glu	Leu	Glu	Ser	Gln	Arg	Glu	Leu	Leu	Leu	Asp	Leu	Ala	Lys	
188					35				40						45		
190	Arg	Ser	Ile	Leu	Asp	Lys	Leu	His	Leu	Thr	Gln	Arg	Pro	Thr	Leu	Asn	
191					50				55						60		
193	Arg	Pro	Val	Ser	Arg	Ala	Ala	Leu	Arg	Thr	Ala	Leu	Gln	His	Leu	His	
194					65				70						75		
196	Gly	Val	Pro	Gln	Gly	Ala	Leu	Leu	Glu	Asp	Asn	Arg	Glu	Gln	Glu	Cys	
197					85				90						95		
199	Glu	Ile	Ile	Ser	Phe	Ala	Glu	Thr	Gly	Leu	Ser	Thr	Ile	Asn	Gln	Thr	
200					100				105						110		
202	Arg	Leu	Asp	Phe	His	Phe	Ser	Ser	Asp	Arg	Thr	Ala	Gly	Asp	Arg	Glu	
203					115				120						125		
205	Val	Gln	Gln	Ala	Ser	Leu	Met	Phe	Phe	Val	Gln	Leu	Pro	Ser	Asn	Thr	
206					130				135						140		
208	Thr	Trp	Thr	Leu	Lys	Val	Arg	Val	Leu	Val	Leu	Gly	Pro	His	Asn	Thr	
209					145				150						155		
211	Asn	Leu	Thr	Leu	Ala	Thr	Gln	Tyr	Leu	Leu	Glu	Val	Asp	Ala	Ser	Gly	
212					165				170						175		
214	Trp	His	Gln	Leu	Pro	Leu	Gly	Pro	Glu	Ala	Gln	Ala	Ala	Cys	Ser	Gln	
215					180				185						190		
217	Gly	His	Leu	Thr	Leu	Glu	Leu	Val	Leu	Glu	Gly	Gln	Val	Ala	Gln	Ser	
218					195				200						205		
220	Ser	Val	Ile	Leu	Gly	Gly	Ala	Ala	His	Arg	Pro	Phe	Val	Ala	Ala	Arg	
221					210				215						220		
223	Val	Arg	Val	Gly	Gly	Lys	His	Gln	Ile	His	Arg	Arg	Gly	Ile	Asp	Cys	
224					225				230						235		
226	Gln	Gly	Gly	Ser	Arg	Met	Cys	Cys	Arg	Gln	Glu	Phe	Phe	Val	Asp	Phe	
227					245				250						255		
229	Arg	Glu	Ile	Gly	Trp	His	Asp	Trp	Ile	Ile	Gln	Pro	Glu	Gly	Tyr	Ala	
230					260				265						270		
232	Met	Asn	Phe	Cys	Ile	Gly	Gln	Cys	Pro	Leu	His	Ile	Ala	Gly	Met	Pro	
233					275				280						285		

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235 Gly Ile Ala Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
236 290 295 300
238 Asn Thr Ala Ala Gly Thr Thr Gly Gly Ser Cys Cys Val Pro Thr
239 305 310 315 320
241 Ala Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
242 325 330 335
244 Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
245 340 345 350

248 (2) INFORMATION FOR SEQ ID NO: 3:

- 250 (i) SEQUENCE CHARACTERISTICS:
 - 251 (A) LENGTH: 1558 base pairs
 - 252 (B) TYPE: nucleic acid
 - 253 (C) STRANDEDNESS: single
 - 254 (D) TOPOLOGY: linear

W--> 256 (ii) MOLECULE TYPE: DNA

259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

261	AAGGAGTCAT	GCCAGTCGGA	GGTCAGTCAC	ATTCTCTCCA	GGGTCCCTGG	TGCCAGGAC	60
262	AGAGTTGAAG	CACTCCCCTT	GAGACCCCTGA	ATATAGGCTT	TGGGTCTTT	AAGGAGGCTA	120
263	TCCTCCAGCA	ATGGCCTCCT	CCTTGCTCCT	GGCTCTTCTG	TTCCTGACTC	CAACCACAGT	180
264	AGTGAACCCC	AAAAGTGAGG	GTCCATGCC	AGCATGTTGG	GGTGCCATCT	TTGACCTGGGA	240
265	GAGCCAGCGG	GAGCTGCTTC	TCGATTTGGC	CAAGAAAAGT	ATCCTGGACA	AGCTGCACCT	300
266	CAGCCAGCGC	CCCATACTCA	GTCGGCCAGT	GTCCAGAGGG	GCTCTCAAGA	CCGCGCTGCA	360
267	GCGCCTCCGC	GGGCCTCGAC	GGGAAACCC	GTTGGAGCAT	GACCAGAGAC	AAGAAGAATA	420
268	TGAGATCATC	AGCTTGCTG	ACACAGACCT	CTCCAGCATC	AACCAGACCC	GGCTCGAGTT	480
269	CCACTTCTCT	GGTAGAACATGG	CCAGTGGCAT	GGAGGTCCGG	CAGACCCGCT	TCATGTTCTT	540
270	CGTGCAGTTC	CCCCACAATG	CCACCCAGAC	CATGAATATA	AGAGTTCTTG	TGCTAAGACC	600
271	ATATGACACC	AACCTCACCT	TGACAAGTCA	GTACGTGGTG	CAGGTGAATG	CCAGTGGCTG	660
272	GTACCAAGCTT	CTCCTGGGAC	CTGAAGCTCA	AGCTGCTTGC	AGCCAGGGAC	ACCTTACTCT	720
273	GGAGCTGGTA	CCAGAAAGCC	AGGTGGCCCA	CAGTTCCCTG	ATCCTGGGCT	GGTTTCCC	780
274	CAGGCCTTTT	GTGGCAGCCC	AGGTAAGGGT	TGAGGGCAAG	CATCGGGTTC	GCCGGCGAGG	840
275	TATCGATTGC	CAGGGGGGGT	CCAGGATGTG	CTGTCGACAA	GAGTTTTTG	TAGACTTCCG	900
276	TGAGATTGGC	TGGAATGACT	GGATCATCCA	GCCTGAAGGC	TATGCCATGA	ACTTCTGCAC	960
277	TGGGCAGTGC	CCACTACATG	TGGCAGGCAT	GCCTGGCATC	TCTGCCTCCT	TTCACACTGC	1020
278	AGTGCTGAAT	CTGCTCAAAG	CCAACGCAGC	TGCTGGCACC	ACTGGCAGGG	GCTCGTGTG	1080
279	CGTGCCTACA	TCTCGCGCC	CTCTGTCTT	GCTCTACTAT	GACAGGGACA	GCAACATTGT	1140
280	CAAGACGGAT	ATACCTGACA	TGGTGGTCGA	GGCCTGCGGG	TGTAGTTAGC	TTATGGGTGA	1200
281	TACAGGCTGC	CTGAGGTAGA	ATGGCCTTCC	TCAGGAAGGG	AAACTCTGTT	CCCACTTCTG	1260
282	TCCAGAATGG	AAACACCTT	CTAACGATGC	AGACATCCCT	CTGTGGACTT	CAGGGGATCC	1320
283	ACCTCTAAAG	AGAGTCACTA	GTGACCAACA	GCCTTTCTCT	CTCCTGGGAC	ATGGTTGACC	1380
284	CAGTACACCC	ATCCTCAGCC	TTAAGTTAGA	GGCTAATCGA	CTCCTACATA	TATATGTCA	1440
285	TTTGTCTCTAG	CAAACACCCC	TTAGCTCCCC	TTAGTCAACT	ATGTAATCTA	CTCTGCCTCC	1500
286	CTGACCCCTGC	CACCGGAAGG	TTCCTATTCC	ACGATGATAT	GCCTTAGTGT	CTCCCCTT	1558

288 (2) INFORMATION FOR SEQ ID NO: 4:

- 289 (i) SEQUENCE CHARACTERISTICS:
 - 290 (A) LENGTH: 352 amino acids
 - 291 (B) TYPE: amino acid
 - 292 (C) STRANDEDNESS: single
 - 293 (D) TOPOLOGY: linear
- 295 (ii) MOLECULE TYPE: peptide

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299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 301 Met Ala Ser Ser Leu Leu Leu Ala Leu Leu Phe Leu Thr Pro Thr Thr
 302 1 5 10 15
 304 Val Val Asn Pro Lys Thr Glu Gly Pro Cys Pro Ala Cys Trp Gly Ala
 305 20 25 30
 307 Ile Phe Asp Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
 308 35 40 45
 310 Lys Ser Ile Leu Asp Lys Leu His Leu Ser Gln Arg Pro Ile Leu Ser
 311 50 55 60
 313 Arg Pro Val Ser Arg Gly Ala Leu Lys Thr Ala Leu Gln Arg Leu Arg
 314 65 70 75 80
 316 Gly Pro Arg Arg Glu Thr Leu Leu Glu His Asp Gln Arg Gln Glu Glu
 317 85 90 95
 319 Tyr Glu Ile Ile Ser Phe Ala Asp Thr Asp Leu Ser Ser Ile Asn Gln
 320 100 105 110
 322 Thr Arg Leu Glu Phe His Phe Ser Gly Arg Met Ala Ser Gly Met Glu
 323 115 120 125
 325 Val Arg Gln Thr Arg Phe Met Phe Val Gln Phe Pro His Asn Ala
 326 130 135 140
 328 Thr Gln Thr Met Asn Ile Arg Val Leu Val Leu Arg Pro Tyr Asp Thr
 329 145 150 155 160
 331 Asn Leu Thr Leu Thr Ser Gln Tyr Val Val Gln Val Asn Ala Ser Gly
 332 165 170 175
 334 Trp Tyr Gln Leu Leu Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
 335 180 185 190
 337 Gly His Leu Thr Leu Glu Leu Val Pro Glu Ser Gln Val Ala His Ser
 338 195 200 205
 340 Ser Leu Ile Leu Gly Trp Phe Ser His Arg Pro Phe Val Ala Ala Gln
 341 210 215 220
 343 Val Arg Val Glu Gly Lys His Arg Val Arg Arg Arg Gly Ile Asp Cys
 344 225 230 235 240
 346 Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
 347 245 250 255
 349 Arg Glu Ile Gly Trp Asn Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
 350 260 265 270
 352 Met Asn Phe Cys Thr Gly Gln Cys Pro Leu His Val Ala Gly Met Pro
 353 275 280 285
 355 Gly Ile Ser Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
 356 290 295 300
 358 Asn Ala Ala Ala Gly Thr Thr Gly Arg Gly Ser Cys Cys Val Pro Thr
 359 305 310 315 320
 361 Ser Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
 362 325 330 335
 364 Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
 365 340 345 350
 368 (2) INFORMATION FOR SEQ ID NO: 5:
 370 (i) SEQUENCE CHARACTERISTICS:
 371 (A) LENGTH: 18 base pairs
 372 (B) TYPE: nucleic acid

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/684,383

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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L:890 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
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L:943 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
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